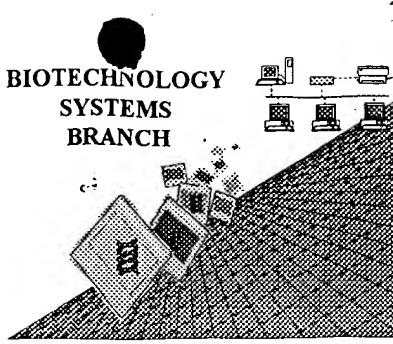


#8/S  
4/20-01

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/424,028  
Source: 16Sb  
Date Processed by STIC: 3/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED  
MAY 29 2001  
TECH CENTER 1600/2600

# Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/424,028</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.  <i>1/4-19</i>	
12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:37

Does Not Comply  
Corrected Diskette Needed

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

*see pg 1-4*

3 <110> APPLICANT: John Bridgham, Michael C. Pallas, Sydney Brenner, Kevin Corcoran, George Golda

W--> 5 <120> TITLE OF INVENTION: Planar Arrays of Microparticle-Bound Polynucleotides

W--> 6 <130> FILE REFERENCE: 815

W--> 7 <140> CURRENT APPLICATION NUMBER: US 09/424,028

W--> 8 <141> CURRENT FILING DATE: 1999-11-16

W--> 9 <150> PRIOR APPLICATION NUMBER: US 08/862,610

W--> 10 <151> PRIOR FILING DATE: 1997-05-23

W--> 11 <160> NUMBER OF SEQ ID: 19

W--> 12 <170> SOFTWARE: Microsoft Word97

W--> 14 <210> SEQ ID NO: 1

W--> 15 <211> LENGTH: 78

W--> 16 <212> TYPE: DNA

W--> 17 <213> ORGANISM: Artificial Sequence

W--> 18 <220> FEATURE:

W--> 19 <221> NAME/KEY: any of a, c, g, t, or u at indicated position

W--> 20 <222> LOCATION: 26-57

W--> 21 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 22 <400> SEQUENCE: 1

*do not put this response  
on <221> line; it  
goes on <223> line;  
<221> responses  
are found in*

*WIPO STANDARD ST.25,  
Appendix 2, Tables  
5 and 6*

W--> 23 actaatcgta tcactattta attaaannnn nnnnnnnnnnn

40

78

W--> 24 nnnnnnnnnn nnnnnnnnggt ttttttttt ttttttv

W--> 27 <210> SEQ ID NO: 2

17

28 <211> LENGTH: 17

29 <212> TYPE: DNA

30 <213> ORGANISM: Artificial Sequence

W--> 31 <220> FEATURE:

32 <223> OTHER INFORMATION: Adaptor.

W--> 33 <400> SEQUENCE: 2

17

34 ataggggctc tcggtag

35 <210> SEQ ID NO: 3

36 <211> LENGTH: 19

37 <212> TYPE: DNA

38 <213> ORGANISM: Artificial Sequence

W--> 41 <220> FEATURE:

42 <223> OTHER INFORMATION: Adaptor.

W--> 43 <400> SEQUENCE: 3

19

44 gatcagctgc tgcaaattt

45 <210> SEQ ID NO: 4

46 <211> LENGTH: 30

47 <212> TYPE: DNA

48 <213> ORGANISM: Artificial Sequence

W--> 50 <220> FEATURE:

W--> 51 <221> NAME/KEY: any of a, c, g, t, or u at indicated position

52 <222> LOCATION: 2-4

53 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 54 <400> SEQUENCE: 4

30

W--> 55 annntacagc tgcatccctt ggccgctgagg

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:38

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

58 <210> SEQ ID NO: 5  
 59 <211> LENGTH: 30  
 60 <212> TYPE: DNA *item 12*  
 61 <213> ORGANISM: Artificial Sequence  
 W--> 62 <220> FEATURE:  
 W--> 63 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 64 <222> LOCATION: 1, 3-4  
 65 <223> OTHER INFORMATION: a, c, g, t, or u  
 W-> 66 <400> SEQUENCE: 5  
 W-> 67 nnntacagc tgcattccctg ggcctgttaag 30  
 69 <210> SEQ ID NO: 6  
 70 <211> LENGTH: 30  
 71 <212> TYPE: DNA *item 12*  
 72 <213> ORGANISM: Artificial Sequence  
 W--> 73 <220> FEATURE:  
 W--> 74 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 75 <222> LOCATION: 2-4  
 76 <223> OTHER INFORMATION: a, c, g, t, or u  
 W-> 77 <400> SEQUENCE: 6  
 W-> 78 cnntacagc tgcattccctt gacgggtctc 30  
 80 <210> SEQ ID NO: 7  
 81 <211> LENGTH: 30  
 82 <212> TYPE: DNA *item 12*  
 83 <213> ORGANISM: Artificial Sequence  
 W--> 84 <220> FEATURE:  
 W--> 85 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 86 <222> LOCATION: 1, 3-4  
 87 <223> OTHER INFORMATION: a, c, g, t, or u  
 W-> 88 <400> SEQUENCE: 7  
 W-> 89 ncnnntacagc tgcattccctg cccgcacagt 30  
 91 <210> SEQ ID NO: 8  
 92 <211> LENGTH: 30  
 93 <212> TYPE: DNA *item 12*  
 94 <213> ORGANISM: Artificial Sequence  
 W--> 95 <220> FEATURE:  
 W--> 96 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 97 <222> LOCATION: 2-4  
 98 <223> OTHER INFORMATION: a, c, g, t, or u  
 W-> 99 <400> SEQUENCE: 8  
 W-> 100 gnnntacagc tgcattccctt cgccctggac 30  
 102 <210> SEQ ID NO: 9  
 103 <211> LENGTH: 30  
 104 <212> TYPE: DNA *item 12*  
 105 <213> ORGANISM: Artificial Sequence  
 W--> 106 <220> FEATURE:  
 W--> 107 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 108 <222> LOCATION: 1, 3-4  
 109 <223> OTHER INFORMATION: a, c, g, t, or u  
 W-> 110 <400> SEQUENCE: 9

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001

TIME: 14:53:38

Input Set : A:\ES.txt

Output Set: N:\CRF3\03212001\I424028.raw

OK 111 ngnntacagc tgc~~atccctg~~ atccgctagc 30  
 113 <210> SEQ ID NO: 10  
 114 <211> LENGTH: 30  
 115 <212> TYPE: DNA *item 12*  
 116 <213> ORGANISM: Artificial Sequence

W--> 117 <220> FEATURE:  
 W--> 118 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 119 <222> LOCATION: 2-4  
 120 <223> OTHER INFORMATION: a, c, g, t, or u

OK 121 <400> SEQUENCE: 10  
 122 tnnntacagc tgc~~atccctt~~ ccgaaccgc 30  
 124 <210> SEQ ID NO: 11  
 125 <211> LENGTH: 30  
 126 <212> TYPE: DNA *item 12*  
 127 <213> ORGANISM: Artificial Sequence

W--> 128 <220> FEATURE:  
 W--> 129 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 130 <222> LOCATION: 1, 3-4  
 131 <223> OTHER INFORMATION: a, c, g, t, or u

OK 132 <400> SEQUENCE: 11  
 133 ntntacagc tgc~~atccctg~~ agggggatag 30  
 135 <210> SEQ ID NO: 12  
 136 <211> LENGTH: 30  
 137 <212> TYPE: DNA *item 12*  
 138 <213> ORGANISM: Artificial Sequence

W--> 139 <220> FEATURE:  
 W--> 140 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 141 <222> LOCATION: 1-2, 4  
 142 <223> OTHER INFORMATION: a, c, g, t, or u

OK 143 <400> SEQUENCE: 12  
 144 nnantacagc tgc~~atccctt~~ cccgctacac 30  
 146 <210> SEQ ID NO: 13  
 147 <211> LENGTH: 30  
 148 <212> TYPE: DNA *item 12*  
 149 <213> ORGANISM: Artificial Sequence

W--> 150 <220> FEATURE:  
 W--> 151 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 152 <222> LOCATION: 1-3  
 153 <223> OTHER INFORMATION: a, c, g, t, or u

OK 154 <400> SEQUENCE: 13  
 155 nnat~~ata~~cagc tgc~~atccctg~~ actccccgag 30  
 157 <210> SEQ ID NO: 14  
 158 <211> LENGTH: 30  
 159 <212> TYPE: DNA *item 12*  
 160 <213> ORGANISM: Artificial Sequence

W--> 161 <220> FEATURE:  
 W--> 162 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 163 <222> LOCATION: 1-2, 4  
 164 <223> OTHER INFORMATION: a, c, g, t, or u

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001

TIME: 14:53:38

Input Set : A:\ES.txt

Output Set: N:\CRF3\03212001\I424028.raw

W--> 165 <400> SEQUENCE: 14  
 W--> 166 nnctacagc tgcattccctg tgttgcgcgg 30  
 168 <210> SEQ ID NO: 15  
 169 <211> LENGTH: 30  
 170 <212> TYPE: DNA  
 171 <213> ORGANISM: Artificial Sequence item 12

W--> 172 <220> FEATURE:  
 W--> 173 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 174 <222> LOCATION: 1-3  
 175 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 176 <400> SEQUENCE: 15  
 W--> 177 nnctacagc tgcattccctc tacaggcg 30  
 179 <210> SEQ ID NO: 16  
 180 <211> LENGTH: 30  
 181 <212> TYPE: DNA  
 182 <213> ORGANISM: Artificial Sequence item 12

W--> 183 <220> FEATURE:  
 W--> 184 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 185 <222> LOCATION: 1-2, 4  
 186 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 187 <400> SEQUENCE: 16  
 W--> 188 nnntacagc tgcattccctg tcgcgtcg 30  
 190 <210> SEQ ID NO: 17  
 191 <211> LENGTH: 30  
 192 <212> TYPE: DNA  
 193 <213> ORGANISM: Artificial Sequence item 12

W--> 194 <220> FEATURE:  
 W--> 195 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 196 <222> LOCATION: 1-3  
 197 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 198 <400> SEQUENCE: 17  
 W--> 199 nnntacagc tgcattccctc ggagcaacct 30  
 201 <210> SEQ ID NO: 18  
 202 <211> LENGTH: 30  
 203 <212> TYPE: DNA  
 204 <213> ORGANISM: Artificial Sequence item 12

W--> 205 <220> FEATURE:  
 W--> 206 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 207 <222> LOCATION: 1, 2, 4  
 208 <223> OTHER INFORMATION: a, c, g, t, or u

W--> 209 <400> SEQUENCE: 18  
 W--> 210 nnntacagc tgcattccctg gtgaccgtag 30  
 212 <210> SEQ ID NO: 19  
 213 <211> LENGTH: 30  
 214 <212> TYPE: DNA  
 215 <213> ORGANISM: Artificial Sequence item 12

W--> 216 <220> FEATURE:  
 W--> 217 <221> NAME/KEY: any of a, c, g, t, or u at indicated position  
 218 <222> LOCATION: 1-3

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:38

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

219 <223> OTHER INFORMATION: a, c, g, t, or u

220 <400> SEQUENCE: 19

221 nnnttacagc tgcatccctc ccctgtcgga

30

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001

TIME: 14:53:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\03212001\I424028.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:7 M:283 W: Missing Blank Line separator, <140> field identifier  
L:11 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <220> field identifier  
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:22 M:283 W: Missing Blank Line separator, <400> field identifier  
L:23 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:24 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:41 M:283 W: Missing Blank Line separator, <220> field identifier  
L:43 M:283 W: Missing Blank Line separator, <400> field identifier  
L:50 M:283 W: Missing Blank Line separator, <220> field identifier  
L:51 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:63 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:66 M:283 W: Missing Blank Line separator, <400> field identifier  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:73 M:283 W: Missing Blank Line separator, <220> field identifier  
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:77 M:283 W: Missing Blank Line separator, <400> field identifier  
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:84 M:283 W: Missing Blank Line separator, <220> field identifier  
L:85 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:88 M:283 W: Missing Blank Line separator, <400> field identifier  
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:95 M:283 W: Missing Blank Line separator, <220> field identifier  
L:96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:99 M:283 W: Missing Blank Line separator, <400> field identifier  
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:106 M:283 W: Missing Blank Line separator, <220> field identifier  
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:110 M:283 W: Missing Blank Line separator, <400> field identifier  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:117 M:283 W: Missing Blank Line separator, <220> field identifier  
L:118 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:121 M:283 W: Missing Blank Line separator, <400> field identifier  
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:128 M:283 W: Missing Blank Line separator, <220> field identifier  
L:129 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:132 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:139 M:283 W: Missing Blank Line separator, <220> field identifier  
L:140 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:143 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/424,028

DATE: 03/21/2001  
TIME: 14:53:39

Input Set : A:\ES.txt  
Output Set: N:\CRF3\03212001\I424028.raw

L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:150 M:283 W: Missing Blank Line separator, <220> field identifier  
L:151 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:154 M:283 W: Missing Blank Line separator, <400> field identifier  
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:161 M:283 W: Missing Blank Line separator, <220> field identifier  
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:165 M:283 W: Missing Blank Line separator, <400> field identifier  
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:172 M:283 W: Missing Blank Line separator, <220> field identifier  
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:176 M:283 W: Missing Blank Line separator, <400> field identifier  
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:183 M:283 W: Missing Blank Line separator, <220> field identifier  
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:187 M:283 W: Missing Blank Line separator, <400> field identifier  
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:194 M:283 W: Missing Blank Line separator, <220> field identifier  
L:195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
L:198 M:283 W: Missing Blank Line separator, <400> field identifier  
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:205 M:283 W: Missing Blank Line separator, <220> field identifier  
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
L:209 M:283 W: Missing Blank Line separator, <400> field identifier  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:216 M:283 W: Missing Blank Line separator, <220> field identifier  
L:217 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
L:220 M:283 W: Missing Blank Line separator, <400> field identifier  
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19